

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_p1\_vs\_p2n model

Run on: October 19, 2002, 07:52:31 ; Search time 1919 Seconds

(without alignments) 4994.452 Million cell updates/sec

Title: US-09-807-459-2

Perfect score: 2359  
Sequence: 1 MAPSDSGDVTKLIAASES.....DPSKALIRKVSTEADNLLEK 458

Scoring table: BLOSUM62

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Ygapop	10.0	Ygapext	0.5
Rgapop	6.0	Rgapext	7.0
Delop	6.0	Delext	7.0

Searched: 1797656 seqs, 1046268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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29: em\_vl:\*
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31: em\_hg\_inv:\*
32: em\_htg\_other:\*
33: em\_htg\_oInv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	Query	DB ID	Description
1	2359	100.0	1810	3 AB017700	AB017700 Babesia c	
2	2355	99.8	1943	3 AF092736	AF092736 Babesia c	
3	995.5	42.2	1542	6 AF16430	AF16430 (Lambda Emb	
4	831.5	35.2	2089	3 AF030060	AF030060 Babesia b	
5	831.5	35.2	2306	3 AF030058	AF030058 Babesia b	
6	830.5	35.2	2323	3 AF030061	AF030061 Babesia b	
7	827.5	35.1	1962	3 BB05MMER	BB05MMER	
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#### ALIGNMENTS

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LOCUS AB017700 Babesia caballi pbc48/31 mRNA for 48kDa merozoite antigen, complete
DEFINITION cds.
ACCESSION AB017700
VERSION AB017700_1 GI:5821173
KEYWORDS 48kDa merozoite antigen; BC48/31.
SOURCE Babesia caballi (strain:USDA) cDNA to mRNA.
```

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RESULT 1
LOCUS AB017700 Babesia caballi pbc48/31 mRNA for 48kDa merozoite antigen, complete
DEFINITION cds.
ACCESSION AB017700
VERSION AB017700_1 GI:5821173
KEYWORDS 48kDa merozoite antigen; BC48/31.
SOURCE Babesia caballi (strain:USDA) cDNA to mRNA.
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REPORT	2			Db	329	GTCGTCGAACTTCGGGGCATTTGACTCAGTCCGAGGGACTACTCGAT	388	
LOCUS	KF092736	AF092736	1943 bp mRNA linear	INV 29-JUN-1999	QY	61	AlaSerValSerAlaTyrmeterArgCysAlaLysGlnAspCysLeuThrLeuGlnSer	80
DEFINITION	Babesia caballi clone x6 rhopty-associated protein 1 (RAP-1) mRNA, complete cds	AF092736		Db	389	GCCTCCGGTAGGCCATACATGAGTCGCTGGCAGAACAGACTGCCATAGT	448	
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ORGANISM	Babesia caballi; Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;			Db	509	GAGGCCSCTTATATACTCTCAAGGAGTGACGTGACCTATGCCCAATAGCTGAG	568	
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AUTHORS	Kappmeyer, L.S. and Knowles, D.P.			Db	569	TGGCTCTCGATGGCTTACAGTGCAGTCGCTGGCCTGAGCTGACTCTCCAAAGT	628	
TITLE	Hennager, S.G. and Knowles, D.P.			QY	141	AspLeuIeGluLysAsnValThrArgAspAlaAspAlaThrAspIleGluasnPheAla	160	
JOURNAL	Detection of equine antibodies to babesia caballi by recombinant B. caballi rhopty-associated protein 1 in a competitive-inhibition enzyme-linked immunosorbent assay			Db	629	AATCTGCTGAGGAGAACTGTACTCGCGAGATGCTACTGAGACTTGTGAGCTTG	688	
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PUBMED	9924470			Db	689	TCCAGGTAACCTGACAGGCCACGCTTACTCAAGAGCTACAGTACAGTGTGACTTC	748	
2 (bases 1 to 1943)				QY	181	GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyLys	200	
AUTHORS	Kappmeyer, L.S. and Knowles, D.P.			Db	749	GGCTCTAGCTCTCTTACAGTGCCTCTACTGGGTGTCGCTGGGCATCACAG	808	
TITLE	Direct Submission			QY	201	ArgAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAspIleGlyTrhLysSer	220	
JOURNAL	Submitted (18-SEP-1998) Agricultural Research Service, US Department of Agriculture, 337 Buctad Hall, Washington, State University, Pullman, WA 99164-7030, USA			Db	809	AGGCACATTAAGCAGATTTTCGCTCTACCTGCCCCCTGACATGGCACAGACAG	688	
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 ORGANISM Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;  
 Babesia. 1 (bases 1 to 1542)  
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 AUTHORS B. B. B. B.  
 TITLE Patent: WO 9314201-A 8 22-JUL-1993;  
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		GlulearLysProserlysAlaLysLysGluileargLysVal		
		GlulearLysProserlysAlaLysLysGluileargLysVal		
Db	1543	ACTGTGGCCAACCTACAAAGGATTCTGAACGGGACTTTAGAA	1602	
Oy	455	Ieu 455		
		Ieu 455		
Db	1603	TTA 1605		
RESULT 6				
LOCUS	AF030061	2323 bp	DNA	linear INV 13-NOV-1997
DEFINITION	Babesia bovis strain Ur	rhoptry	associated	protein-1 (rap-1) gene,
SOURCE	complete cds.			
ACCESSION	AF030061			
VERSION	AF030061.1	GI:2613068		
KEYWORDS				
ORGANISM	Babesia bovis			
Babesia bovis.	Babesia bovis.			
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;	Babesia bovis.			
Babesia.	Babesia bovis.			
REFERENCE	1 (bases 1 to 2323)			
AUTHORS	Suarez, C.E., Palmer, G.H., Hotzel, I. and McElwain, T.F.			
TITLE	Structure, sequence, and transcriptional analysis of the Babesia bovis rap-1 multigene locus			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 2323)			
AUTHORS	Suarez, C.E., Palmer, G.H., Hotzel, I. and McElwain, T.F.			
TITLE	Direct Submission			
JOURNAL	Submitted (17-Oct-1997) Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164, USA			
FEATURES	source			
	/organism="Babesia bovis"			
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	1. .223			

AUTHORS	Mishra, V.-S., Stephens, E.B., Dame, J.B., Perryman, L.E., McGuire, T.C.
TITLE	Immunogenicity and sequence analysis of recombinant p58: A neutralization sensitive, antigenically conserved Babesia bigemina merozoite surface protein
JOURNAL	Mol. Biochem. Parasitol. 47, 207-212 (1991)
MEDLINE	92049553
FEATURES	Location/Qualifiers
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ORIGIN	US-09-807-459-2 (1-458) x BB058MER (1-1962)
Alignment Scores:	Pred. No.: 7e-58 Length: 1962 Score: 827.50 Matches: 181 Percent Similarity: 59.12% Conservative: 75 Best Local Similarity: 41.80% Mismatches: 140 Query Match: 35.08% Indels: 37 DB: 3 12 Gaps: 12
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Qy	398 -----IleAsnAsnGluIleArgLysProSerLysAlaLeuIleArgLysAla 415
Db	1478 AAAGTCCTGAGTGAACAACTGCTCAACCTGCCAACATACTAGTCAGTTGGACA 1537
Qy	416 GluAlaAspAspLeuPheGluasnlysIleGlyGlnGlyThrValAspPheIleAsnys 435
Db	1538 GGCCGCCAGAAAT--TCATTCGGCACCCATGAGGTACTAGCAGTCCTRAAGCA 1594
Qy	436 GluIleArgAspProSerLysAlaLeuIleArg---LysValSerThrGluAlaAspAsn 454
Db	1595 ACTGTTGGCCAACCTACAAAGAATTCTGAACGGAGCTTTAGAAACACTAAAGACGCA 1654
Qy	455 Leu 455
Db	1655 TTA 1657
RESULT	7
BBO58MER	BB058MER 1962 bp linear INV 28-APR-1995
LOCUS	B.bigemina merozoite surface protein (p58) gene, complete cds.
DEFINITION	B.bigemina merozoite surface protein (p58) gene, complete cds.
ACCESSION	M60378
VERSION	M60818..1 GI:155860
KEYWORDS	merozoite surface protein.
SOURCE	Babesia bigemina merozoite DNA.
ORGANISM	Babesia bigemina Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
REFERENCE	1 Babesia 1 to 1962)

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QY	184 PhePheAspLysLeuSerPheThrThrGlyLeuPheGlyLrpGlyLysAlaLeu	203	Alignment Scores:
Db	798 TTCTTCACAACTAACGCTTGCTTCACACTGCCTGCTGTTGGTTGGATCCAGAAGCGCTTG	857	Pred. No.: 7e-58
QY	204 LysGlnIleLeuArgSerAsnLeuProLeuAspIleGlyLrpGlyLysAlaLeu	223	Score: 827.50
Db	858 AAGCTTGCTGCTAGAGCACTTCGGTACCGTGAACC	914	Percent Similarity: 59.12%
QY	224 LeuGlnHistLeuSerSerTyrlsAspTyrmEtaPheGlyLrpGlyLysAlaLeu	243	Best Local Similarity: 41.80%
Db	915 ATCCGGAAATAGCTAGCTGGCTACGCCGAGCTACATGACCTGCGCTGAC	974	Query Match: 35.08%
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QY	264 TyrValAspThrProTrpTyrlsPhePheAsnLysGluLeuPheGlyLrpGlyLysAlaLeu	283	QY 4 SerAspSerValGlyAspValThrLysThrIleLeuAlaAlaSerGluSerValAspSer 23
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QY	303 AlaLeuLysGlyLysValSerThrAspThrLysAspLeuPheGlyLysAlaLeu	302	QY 24 AlaAlaAsnAlaTyroMetIleAsnSerAspMetSerAspTyrmLeuSerAlaValSerAsp 43
QY	323 GlyIleValAspPheAsnLysGluIleArgAspProSerLysAlaLeuLysGlyLys	342	Db 342 GAAATGGAAGCAACTCAGGTCACAAAGATATGCAAAAGTCATGCTAATGTTAGAG 401
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QY	343 ValSerAsnAspAlaLysAspLeuPheGluAsnIleLeuGlnSerGluAsnIleLeu	356	Db 402 ACCATGTTGGTGGAGCTGCTGGAGAAGTGTGTTAACTCTACCGCTGAGACGCTGA 461
Db	1266 -----OCTAGCCAACTAAATTCCGAGAAGCTCTACCTTCTCAGCA 1315		QY 64 SerAlaTyrmMetSerargCysAlaLysGlnAspCysLeuIleLeuGlnSerIleLysTyr 83
QY	357 GlnglyIleValAspPheAsnIleAsnAsnGluIleArgAsp-----ProSerLysAlaLeu	374	Db 462 ATTGCCPATGTTAACCGTTCATGAGGGCATTGTCAGCAGCATG----- 515
Db	1317 AGGGAGCCCTGAGCACCGTGTAGAGCTTAACTCTGTGCGGATAAG-----Gly	1370	QY 84 ProLeuGluAlaLysTyrglnProteauThrLeuProSpProTyrglnLeuGluAlaAla 103
QY	375 IleArgLysValSerThrGlyAlaGluAspLeuPheGlyLysIleGlyIleGlyLys	394	Db 516 -----AAGTCACAGCCGTTGAGCTGCTGCACATCTTACAGTGTGACGCTGC 563
Db	1371 ---CAGAACGGCGACCAACATCCGAGACGCTGTAGAGAACAGCTTCGTCAGC-- 1424		QY 104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrp 123
QY	395 ValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValTyr	414	Db 564 TCTACGTTTCAGGGAAAGTGTACCTGCGAAGATGAGCTGCTG 623
Db	1425 ---GATTCGGCGAAACTGTGATTGAGTCCTGAGAACATAAGTCATGCTGCTACT	1481	QY 124 MetArgPheArgArgLysAsnHisSerTyrmPheHisAspLeuValPheAsnLeu 143
QY	415 Thr-----GluAlaAspAsp 419		Db 624 ATGCGTTCGAG-----ASAGCCCGGCACTACATCTGTTGAGCTG 677
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RESULT 8			Db 678 AAGAACAGATGTTGTTGAGCCTGATCCTGAGACTTCGATCGAGTAC 737
112361	LOCUS 112361	DEFINITION Sequence 1 from patent US 5422428.	DNA linear PAT 26-JUL-1995
ACCESSION	112361	VERSION 1.1	GI:910384
KEYWORDS	SOURCE	ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 1962)	Unclassified.	
AUTHORS	McGuire,T.C., McElwain,T.F., Perryman,L.E. and Davis,W.C.		
TITLE	Immunization against babesioses using purified surface antigens of Babesia bigemina and similar immunogens		
JOURNAL	Patent: US 5422428-A 1-06-JUN-1995;		
FEATURES	Location/Qualifiers		







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Qy 292 -----
CDS
Db 1009 AAAACTATCTGAAAGCCAATGTTGCTGAGCCACTAAAAGTTATGCAGGACACTCAC 1068
Qy 293 -----
Db 1069 GAAAAACCAAAGGTATCTGAAGNGAATGTCAGGCCAACTAAC 306
Qy 307 LysValSerThrAspThrLysAspLeuPheGluAsnLysLysLysGlyLysGlu 1128
Db 1129 GAGGTCTCTAACGTCACCAACACTCTTGATGATAACACTGGCCACCCACCAGAG 1188
Qy 327 PhePheAsnLysGluLeaGaspProSerLysAlaLeuLysGluValSerAsnAsp 326
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Qy 347 AlaValAspIlePheGluAsnLysIleGlyLysGlyLysGluValAsnGlu 366
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Qy 387 GluAsnLysIleGlyLysGlyLysGlyLysGluValSerAsnAsp 346
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Qy 398 -----IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValThr 415
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Qy 436 GluIleArgAspProSerLysAlaLeuIleArg---LysValSerThrGluAlaAspAsn 454
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Qy 455 Leu 455
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RESULT 12
AF030053
LOCUS AF030053          2089 bp   DNA linear INV 13-NOV-1997
DEFINITION Babesia bovis strain S2P rhoptry associated protein-1 (rap-1) gene,
COMPLETE CDS.
ACCESSION AF030053
VERSION AF030053.1 GI:2613052
KEYWORDS SOURCE
ORGANISM Babesia bovis.
Babesia bovis.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
REFERENCE AUTHORS
TITLE 1 (basses 1 to 2009)
Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
SUBTITLE Unpublished
2 (basses 1 to 2009)
Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
SUBTITLE Direct Submission
JOURNAL Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
Washington State University, Pullman, WA 99164, USA
LOCATION/QUALIFIERS
FEATURES source
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/strain=S2P

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BASE COUNT
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Qy 41 ValSerAspAsnHeaLysGluAspLysSerGlnValProLysGlySerAsnOxySer 60
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Qy 61 AlaSerValSerAlaTyMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80
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ACCESSION AF030055

VERSION AF030055.1 GI:2613056

KEYWORDS SOURCE Babesia bovis.

ORGANISM Babesia bovis

Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.

REFERENCE 1 (bases 1 to 2089)

AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.

TITLE Structure, sequence, and transcriptional analysis of the Babesia bovis rap-1 multigene locus

JOURNAL 2 (bases 1 to 2089)

REFERENCE 2 (bases 1 to 2089)

AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.

TITLE Direct Submission

JOURNAL Submitted (17-OCT-1997), Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164, USA

FEATURES source Location/Qualifiers 1. 2089

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BASE COUNT 657 a 447 c 414 g 571 t ORIGIN

Alignment Scores:

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Best Local Similarity:	35.53%	Mismatches:	195
Query Match:	35.04%	Indels:	49
DB:	3	Gaps:	6

US-09-807-459-2 (1-458) x AF030055 (1-2089)

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QY	61	AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeugInser	80
Db	292	GAGGTTAGTAACTATGTAATGATGTTGACGGTTGCAATGTCAGGATGCCCTCAAGTCACCAGAAGCTATA	351
QY	81	LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProLysProSpProTyrGlnLeu	100
Db	352	GTCANATACCGTGTATCAAGATGTCACCTCTATCCTCCAAACCTTACAGTG	411
QY	101	GlutAlaAlaPheLeuPhenylLysGluSerAspAlaAsnProAlaAsnSerThrGluLys	120
Db	412	GATGTCGCTCAGATTGTCAAAGAGTCAGAACCTGCAAGAACAGAGTCATGCCAAAGAACAGCTGAA	471
QY	121	ArgPheTrpMetArgPheArgGlyLysAsnHisSerYrPheHisAspLeuValPhe	140
Db	472	CGCGATGATGATGCTGCGTTGAGAAATGGAGGSAACCTGTTGATTACCACTACTTCGTCAC	531
QY	141	AsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspLeuGluAsnPheAla	160
Db	532	GTCCTGTTGACACATGTCACGGAGAACATCCGAATGTTGAATATCTGTC	591
QY	161	SerArgTyrLeuTyMethAlaThrLeuTyTyrLysThrTyRThrAsnValAspGluPhe	180
Db	592	ACAAAGTACTCTATGCTTACATGACTACAAGACTTATTGACGTTAACAGTAGT	651
QY	181	GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheClyTrpGlyIleLys	200
Db	652	AACGCCAAGTCTCTCAAGATTCAGCTCACTACAAGATTCACTCGTCGTCGTTAGG	711
QY	201	ArgAlaLeuLysGlnIleLeuLysSerAlaLeuProLeuSpileGlyThrGluHisSer	220
Db	712	CAACCATGGTGTATCATCAGGGTGAATGTTCTGAGATTGAAAGGAGAAGGAGAAGGAG	768
QY	221	ValSerArgLeuGlnHistLethrSerSerTyrLysAspTyrMetAspThrGlnIlePro	240
Db	769	ATCGACGACGATCACTCACTACTAGCAGCTACAGATGACGACGCCAGATTC	828
QY	241	AlaLeuProLysPheAlaLysArgPheSerIleLeuMetValValGlnArgLeuLeuAlaThr	260
Db	829	ACTCTTCTCAAGTTRGACGCGCTGTTGACATCGTGAAGAAGGTTCTGCTCGGTAGC	888
QY	261	ValAlaGlyTyrValAspHirProTyrTyrLysLysTrpTyrMetLysLeuLysAsnPhe	280
Db	889	TGACCTCTGACGTGAACTCTCTGAAACATGGATAAGAAATCAGAGACTT	948
QY	281	MetValAsnArgValPheIleProThrLysLysPhe-----	292
Db	949	TTCTCTAAACAGTTACCCACCTACRAAGAAGTCACTAACGAGTCTACC	1008
QY	292	-----	292
Db	1009	AAAACATATCTGAAGGCCATGTCGCCCCACTAAAGTTATGCAAGCACTC	1068
QY	293	-----	-----
Db	1069	AAAAAACCAAAGGCTATCTGAAGAGAATGTCAGCCGAACTACTAACGCTTTCAAG	1128
QY	307	LysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAsp	326
Db	1129	GAGGCTCCCAAGTCACCAACACTCTCTGATGAGAACATTGGCAACCCACCAAGGAG	1188
QY	327	PhePheAsnLysGluLeuArgAspProLysAlaLeuLysGluLysValSerAsnAsp	346
Db	1189	TTTTCAGGGAAAGCTCCCACGCACTAAACATTCCTAGACGAAACATCCTGGTCACCA	1248
QY	347	AlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGlu	366







Db 2632 GTCATAATTCGGTTGATCAAGGTTACCAACCTCTATCTCTTCCAAACCTTACACGTG 2691  
 Qy 101 GluAlaAlaAlaPheIleLeuPhelysGluSerAspAlaAsnProAlaAsnSerThrGluIys 120  
 ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: :::::::::::::  
 Db 2692 GATGCTGGCTCACATTGTCAGAGACTGCAAGAACCTGCCAAGACAGCGTAAG 2751  
 Qy 121 ArgPhePhePheMetArgPheArgArgGlyIysAsnHisSerTerPheHisAspLysValPhe 140  
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 Db 2752 CGCGGATGCTGGCTTCAGAATGGAGCGAACCATGGTGATTAACCACTACTGTCACT 2811  
 Qy 141 AsnLeuLeuGluIysAsnValThrArgAspAlaSpaLeuPheIleAspLeuAspIleAla 160  
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 Db 2812 GGTCCTGTTGAAACACAACAGTTGTCACCGAGGAACATACCGATGTGAAATCTGTC 2871  
 Qy 161 SerArgTrpLeuTrpMetAlaThrLeuTrpTrpLysThrTrpIleAsnValAspGluPhe 180  
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 Db 2872 AACGCCAACGTTCTACATGCTTACCATGAACACTTATGACTAACAGATRG 2931  
 Qy 201 ArgAlaLeuLysGlnIleLeuArgSerAsnLeuProLeuAspIleGlyThrGluHisser 220  
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 Db 2992 CAACATGAGTAGTATCATCAGTGGATGTCAGTGAAGATTT--GAAGAAAGGAGC 3048  
 Qy 221 ValSerArgLeuGlnHisIleThrSerSerTerIlysAspTerMetAspThrGlnIlePro 240  
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 Db 3049 ATGGAACTPATCATCACTCAACTACTGAGCTACGGAGATTACCTGACCGATCCA 3108  
 Qy 241 AlanineProLyseHeAlaLysArgPheSerLeuTerValValGlnIleLeuAlaThr 260  
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 Db 3109 ACTCTTCCAAAGTTGCACTGCAGTCGTTATGCTGACATGGGAAGAGGTTGCTGGTAGC 3168  
 Qy 261 ValAlaGlyTerValAspThrProTrpTerLysLysIlePheIleLeuIysAsnIle 280  
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 Db 3169 TTGACCTGCTACGTTGAAGCTCCCTGGTACAAAGATGGATAAGAAATTGAGATTT 3228  
 Qy 291 MetValAsnArgValPheIlePheThrIysLysIlePheIleLeuIysAsnIle 292  
 Db 3229 TTCTCTAAAAAACGTTACCCAAACCTTACACAAAGTTCATCGAGGATACTAACGGAGTTAC 3288  
 Qy 292 ----- 292  
 Db 3289 AAAAACTATCTGAAAGCCATGTTGCTGAGCCACTAAAGATTTATGCAGGACACTAC 3348  
 Qy 293 ----- 292  
 Db 3349 GAAAAACCAAAGCTACTGTGAAAGAGATGTTGCCGAACTACTAGACTTTTCAG 3408  
 Qy 307 LysValSerThrIspThrIysAspPheIleGluAsnLysIleGlyGlyIlyIleValAsp 326  
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 Db 3409 GAGCTCTCTCAAGCTTACCAACACACTCTGCAAGACATGGCCAACCCACCAAGGAG 3468  
 Qy 327 PheIleAsnLysIleIleAspProSerIleAlaIleLysGluIleAspIleAsnAsp 346  
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 Db 3469 TTCTTCAGGGAAGCTCCCCAACGCAACTAACATTCTCPAGACCAAACTCGCTCAACCA 3528  
 Qy 347 AlanysAspLeuPheGluAsnLysIleGlyGlyIlyIleValAspPheIleAsnAsnGlu 366  
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 Db 3529 ACCAGGGATTCCTC---AGGAGCTCTCACCCATCTAGCCACTCTCTGAGGAGAT 3585  
 Qy 367 IleArgAspProSerIleAlaIleIleArgIysValSerTerIleGluIleAspIle 386  
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 Db 3586 ATTGCTCACCTACTAAAGAATTTCTCAGGATGTTCCCTCAAGTCACCAAGGTATA 3645  
 Qy 387 GluAsnIleIleGlyGlyIlyIleValAspPheIleAsnAsnIleAsnAsnIleAsn 397  
 ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: :::::::::::::  
 Db 3646 ACTGAGAACATGCTCAACCAACTAAAGGTTCTCTAGGAGSTTCCATGCTACCATG 3705  
 Qy 398 ---IleAsnAsnGluIleArgAspProSerIleAsnIleLeuIleIleArgIysValYtrh 415,  
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 Db 3706 AAAGCTCTGATGAAACATGGTCAACTGCCAACGAAARTCATGCTGTTGTCAC 3765

BASE COUNT 766 a 477 c 437 g 642 t 3 others  
 ORIGIN  
 Alignment Scores: 1.25e-57 Length: 2325  
 Pred. No.: 825.50 Matches: 183  
 Score: 51.90% Conservative: 77  
 Percent Similarity: 51.90% Mismatches: 192  
 Best Local Similarity: 36.53% Indels: 49  
 Query Match: 34.99% Gaps: 8

US-09-807-459-2 (1-458) x AF030062 (1-2325)

Qy 416 GluAlaAspAspIlePheGluAsnLysIleGlyGlyIlyIleValAspPheIleAsnLys 435  
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 Db 3766 GGCCCACGAT--TCATTCGGCGCCAGGTCATGACGTTCTTAACGAA 3822  
 Qy 436 GluIleArgAspProSerIysAlaLeuIleArg---LysValSerThrGluIlaAspIle 454  
 ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: :::::::::::::  
 Db 3823 ACTGTTGCCAACCTACAAAGGAATTCTGAAACGGAGCTTGTAGAACTRACTAAAGACGCA 3882  
 Qy 455 Leu 455  
 ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: :::::::::::::  
 Db 3883 TTA 3885

RESULT 18

AF030062 AF030062 2325 bp DNA linear INV 13-Nov-1997  
 DEFINITION Babesia bovis strain R1A rhoptry associated protein-1 (rap-1) gene  
 VERSION AF030062.1 GI:2613070

SOURCE Babesia bovis  
 ORGANISM Babesia bovis  
 Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;

REFERENCE 1 (bases 1 to 2325)  
 AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.  
 TITLE Structure, sequence, and transcriptional analysis of the Babesia bovis rap-1 multigene locus  
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2325)  
 AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-Oct-1997) Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164, USA  
 FEATURES Location/Qualifiers  
 source 1. . 2325  
 /organism="Babesia bovis"  
 /strain="R1A"  
 /db\_xref="taxon:5865"  
 /note="isolated in Argentina"  
 gene 22. . 1720  
 /gene="rap-1"  
 /note="gene copy 1"  
 CDS 22. . 1719  
 /gene="rap-1"  
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 /product="ribozyme associated protein-1"  
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 /db\_xref="GI:2613071"  
 /translation="MRTISGVGCLFLVFSHVSARHNORVGLAPAEVWGLDTSPLEADYLMILRDHHNITKDMKHVLNSNGDQIINDVCSNAPEDSNCREVNIVADRCM  
 YCGFTIDMKVYPLQXOPQPLSPNQYQDAAFRLFKESSNPANPSKSYKRMWLRFGA  
 NSGHDYHVVGLNNVYHGEGTIDVEVLYNKLYMATMYKYLTKLTMNSIMAKFNF  
 SFITKISRRIOITSIIRWNPDEBFRSERITOLISSEDMTIQPILSKR  
 SYADMKVFLGSLSLTSVAPWRKWRKDFSKNTQPQKRFEDDNEPTVYK  
 ANVAEPKFKMOTHEKKGYKVKVNEPTEPKFKEAQPVWKFEDDNEPTVYK  
 EAFOQTKIFLDENIQPTEFREAPQKTFHKTIDENIAQPFEFQDVPQKVKE  
 NTIAQTKIFLDENIQPTEFREAPQKTFHKTIDENIAQPFEFQDVPQKVKE  
 VEQOPTKEELGALETTKDALHIGKSSBEANTYDASENTTOSNDSTSINGEDTAGYL"

QY 1 MetAlaProSerAspSerValGlyAspValThrLeuLeuAlaAlaSerGluSer 20  
   :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
 Db 112 CTCGCTCCAGCTGAACTGCTAGGTGTTAACCTCACATTGGAAACAGCTGATCCTG 171  
 QY 21 ValAspSerAlaLalaAsnAlaAlaMetLeuAsnSerAspMetSerAspTyrLeuSerAla 40  
   :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:  
 Db 172 ATGACTCTCGTGACCCAGATGCRCAACATTACTAGGATATGACATGTTTGAGCAT 231  
 QY 41 ValSerAspAsnPhenAlaGluArgGlycSerGlySerAlaProIysGlySerIysCysSer 60  
   :::|||||:::|||||:::|||||:::|||||:::|||||:  
 Db 232 GCGCGTAGAGCAGATGTAATGATGATGTTGCTCTAATGCTCTCTGAGGACTCCA 291  
 QY 61 AlaSerValSerAlaAlaMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80  
   :::|||||:::|||||:::|||||:::|||||:::|||||:  
 Db 292 GAGGTAGTTAACATTATGCTGACCGTGTGAAATGCTACGATGTTGAAAT 351  
 QY 81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyroGlnLeu 100  
   :::|||||:::|||||:::|||||:::|||||:::|||||:  
 Db 352 GTCAAATACTCCGTGTATCAAGAGTACCCACCTATCTCTCCAAACCTTACACAGT 411  
 QY 101 GluAlaAlaPheIleLeuPheIleAspSerAlaAsnProAlaAsnSerThrGlnLys 120  
   :::|||||:::|||||:::|||||:::|||||:::|||||:  
 Db 412 GATGCTCGGTTCAAGATGTTCAAGAGAGTGTGATCCAACTCTGCTAAGACAGCTAA 471  
 QY 121 ArgPheTerPmetArgPheArgArgGlyAsnNHISerTyrPheHisAspLeuValPhe 140  
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 Db 472 CGCGAATGTTGCGTTCAAGAAATGGAGCAGAACCTGGTGTACACTACTTGCTACT 531  
 QY 141 AsnLeuIeuglLysAsnValThrArgAspAlaSpaAlaThrAspIleGluAsnPhenAla 160  
   :::|||||:::|||||:::|||||:::|||||:  
 Db 532 GGCTCTGTGAAACAACTGTGTCACGGGGAAAGAACTACCGATGTTGATCTCTG 591  
 QY 161 SerArgTyrLeuIyMetAlaLthrLeuIyTyrLysThrTyrThrAsnValAspGluPhe 180  
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 Db 592 AACAAAGGTACTCTATAGTGCCTACCATGACTACAAGACTTATTGACAGTAAACAGTAG 651  
 QY 181 GlyAlaSerPhepheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLys 200  
   :::|||||:::|||||:::|||||:::|||||:  
 Db 652 AACGCCAAGTTTTCACAGATTCAGCTTCACTACAAGATATTCAACCGCTGCTATTAG 711  
 QY 201 ArgAlaLeuLysGlnIleLeuArgSerAlaLeuProLeuAspIleGlyThrGluHisser 220  
   :::|||||:::|||||:::|||||:::|||||:  
 Db 712 CAACATGAGGTGATCATCAGTTGGAAATGTTCTGAGATT---GAAGAAGGGC 768  
 QY 221 ValSerArgLeuGlnNHisIleHsSerSerTyrIlysAspTyrMetAspThrGlnIlePro 240  
   :::|||||:::|||||:::|||||:::|||||:  
 Db 769 ATCGAACGTATCACTCAACTAGCAGCTACAGGAGATTACATGTCAGATCC 828  
 QY 241 AlaLeuProLysPheAlaLysArgPheSerLeuMetAlaValGlnAglieLeuAlaThr 260  
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 Db 829 ACTCTTCTCAAGTTGTCACGTCGTTCTGACATGGAAAGGGTTCTGCTGGTAC 888  
 QY 261 ValAlaGlyTyrValAspThrProTrpTyrIlysTyrTyrMetLysIleuLysAsnDhe 280  
   :::|||||:::|||||:  
 Db 889 TTGACCTCTGTAGCTTGAGGCTCTCTGGACAAAGATAAGAATTCAAGNACTT 948  
 QY 281 MetValAsnArgValPheIleProThrLysPhe----- 292  
   :::|||||:::|||||:  
 Db 949 TCTCTCTAAACACGTATCCAAACCTACAAAGAAGTTCATCGAGGATACTAAC 1008  
 QY 293 -----PheAlaLysGluIleArgIleGluProSerLysAla----- 303  
   :::|||||:::|||||:  
 Db 1009 AAAACTATCTGAAGCCAATGTTGCTGAGGCCACTAAAGATTTATGCAAGGACACTC 1068  
 QY 304 -----LeuIysGluIysValSerThrAspThrAspLeuPheGlu 317  
   :::|||||:::|||||:  
 Db 1069 GAAAACCAAGGCTATCTGAAAGAGATGTTGGCGAACCTACTAGACTTTTCAG 1128  
 QY 318 AsnIysIleGlyGlyGlyIlyThrValAspPhepheAsnLysGluIleArgAspProSerLys 337  
 Db 1129 --GAGGCTCTCAAGTCACCAACACTCTCTGATGAGAACATTTGGCCAACCCACAG 1185  
 QY 338 AlaLeuIysGluIysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlycIn 357

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RESULT 19

BBODNA	BBODNA	DNA	linear	INV	26-APR-1993
LOCUS	BBDNA	2005 bp			
DEFINITION	Babesia bigemina DNA sequence.				
VERSION	M85184				
KEYWORDS					
SOURCE	Babesia bigemina (strain Mexico) merozoite DNA.				
ORGANISM	Babesia bigemina				
REFERENCE	1 (bases 1 to 2005)				
AUTHORS	Mishra,V.S., McElwain,T.F., Dame,J.B. and Stephens,E.B.				
TITLE	Isolation, sequence and differential expression of the p58 gene family of Babesia bigemina				
JOURNAL	Mol. Biochem. Parasitol. 53, 149-158 (1992)				
MEDLINE	92365724				
FEATURES	Location/Qualifiers				
source	1. . 2005 /organism="Babesia bigemina" /strain="Mexico" /db_xref="taxon:3866" /dev_stage="merozoite"				
BASE COUNT	550	a	439 c	478 g	538 t
ORIGIN					

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Percent Similarity:	Conservative:	N mismatches:	Best Local Similarity:	Indels:	Query Match:	Gaps:
4	823.00	2005	174	61.31%	78	129	42.34%	34.89%	3	10
Db:										

US-09-807-459-2 (1-458) x BBODNA (1-2005)

QY	4	SerAspSerValGlyAspValThrIysThrLeuLeuAlaAlaSerGluSerValAspSer	23
Db	282	GGAGGTTGTTGGAGATGTTGCTCCAGACCTCTGCTGGAGGCCAATGAGTTGTCATGT	341
QY	24	AlaAlaAspAlaAlaMetLeuAsnSerAspMetSerAspTyrLeuSerAlaValSerSp	43



	FEATURES	Location/Qualifiers
	Source	/organism="Babesia bigemina" /strain="Mexico"/db_xref="taxon:5866" /dev_stage="merozoite"
Qy	164 LeuTyrMetAlaThrLeuTyrTyrLysThrThrAsnValAspGluPheGlyAlaser 183	
Db	738 TTCTACATGACTAGCTGTTGACTACAGACTAACCTGACCTTACGGCCGTAAG 797	
Qy	184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrPheGlyIleLysArgAlaLeu 203	
Db	798 TTCTCAACAAAGCTTGCTTCACACTCGCTGTCGGTTGGTACGTGAGGCCGTCAG 857	
Qy	204 LysGlnIleLeuArgSerAsnLeuProLeuAspIleGlyTyrPheGlyIleLysArgAlaLeu 203	
Db	858 AAGCGTTGTTAGGCAACCTTCGGTGAACCTGACCTGACCTGGACCTGGAC 914	
Qy	224 LeuGlnHistLeuSerSerTyrLysAspTyrMetAspPheGlyIlePheAlaLeuPro 243	
Db	915 ATCCGGAAATAGCTAGCGCTACCGCAGCATGATGACCGACAGCTGGAC 974	
Qy	244 LysPheAlaLysGlyPheAsnPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly 263	
Db	975 TCGTTCGCCTGGCTTCCTCAACATGGCTACTAACCTGCTGTTGGTTACCGTCAGCGAC 1034	
Qy	264 TyrValAspThrProTrpTyrLysLysPheAsnLeuLysAsnPhMeValAsn 283	
Db	1035 TACGTCATTTGCCCGCGTACAAGGGTGTACAGGAAGTCAGTACGCCAGTGCCTGCGATGACC 1094	
Qy	284 ArgAlaPheIlePheThrLysPhePheAsnLysGluIleArgGluProSerLys--- 302	
Db	1095 --TTCTTACTGACCTGCGCAAGTGTATTGAGCACGCTGCTTCAGCGCTGAAGACT 1151	
Qy	303 AlaLeuLysGluLysValSerThrAspThrLysAspLeuPheGlyIleGlyGln 322	
Db	1152 GCCACACAAAGCTGGTCCCCGAGGACACGGAGCTATCAGAATGTCGGTCAA 1211	
Qy	323 GlyIleValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLys 342	
Db	1212 AGCACCAAGCATAATGCCAAC - GGTGIACTGTCATTGTCACAGATGATAAGGAG--- 1265	
Qy	343 ValSerAsnAspAlaLysAspLeuPheGluAsnIle-----Gly 355	
Db	1266 -----CCTACCCAACAACTAAATTCTGAGAGTCGCTCACTACCTTCTAGGCA 1316	
Qy	357 GluGlyLysValAspPheIleLeuAsnGluIleArgAsp----ProSerLysAla 374	
Db	1317 AAGGAGGCCGTTGAGCACGTTGAGAAGGTTAAATCGTTGTCGGATAAG--- 1370	
Qy	375 IleGlyLysValAspThrGlyAlaGluAspLeuPheGluAsnLysIleGlyGlyIleThr 394	
Db	1371 --CRAAGGGCACCACCACTCGGAAGGAGCTGTAGAGGAACACGTTCCGTCGGC--- 1424	
Qy	395 ValAspPheIleAsnAspGluIleArgAspProSerLysAlaLeuLeuIleArgAsp 414	
Db	1425 --GATTCGGGAAACTGATTGAGGTCCTGAGAACATACTGCGATGCTGCTTACT 1481	
Qy	415 Thr-----GluAlaAspAsp 419	
Db	1482 ACTCGAGGTTAACAGCCGAGAAAGTTGATGCCACGAT 1520	
RESULT 21		
BBONAB	BBONAB	2005 bp
LOCUS	Babesia bigemina	DNA
DEFINITION	Babesia bigemina DNA sequence.	linear
ACCESSION	M5185	INV 26-APR-1993
VERSION	M5185.1	G:1:155878
KEYWORDS	Babesia bigemina (strain Mexico) merozoite DNA.	
SOURCE	Babesia bigemina	
ORGANISM	Babesia bigemina (strain Mexico)	
EBIARYOTA	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.	
REFERENCE	1 (bases 1 to 2005)	
AUTHORS	Mishra,V.S., McElwain,T.F., Dame,J.B. and Stephens, B. B.	
TITLE	Isolation, sequence and differential expression of the p58 gene family of Babesia bigemina	
JOURNAL	Mol. Biochem. Parasitol. 53, 149-158 (1992)	
MEDLINE	92365724	
BASE COUNT	550	a 443 c 480 g 532 t
ORIGIN		
US-09-807-459-2 (1-458) x BBONAB (1-2005)		
Qy	4 SerAspSerValGlyAspValThrLysIleLeuAlaLysSerGluSerValAspSer 23	
Db	282 GCAGAGGTGTTGGAGATGTTCCAGACAGCTTGCTGGCACCAAGGAGTTGTCAGTC 341	
Qy	24 AlaAlaAsnIleAlaMetIleAsnSerAspMetSerAspPheIleAsnSerAlaValSerAsp 43	
Db	342 GAAATGGAAACGAGCTGAGATTAACGAGAATATGAAGATTCAGTGTGCGAGACGTCAGGAG 401	
Qy	44 AsnPheAlaIleGlyIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63	
Db	402 ACCATGGTGTAGTAGGTCGCAAGAACAGGCTTAACGTCGGCCCAACAGCTTA 461	
Qy	64 SerAlaTyrMetSerArgCysAlaLysGluAspCysLeuThrLeuGlnSerLeuLysTyr 83	
Db	462 ATTGCCTATGTTGACGCTTGATGAGGGATGTCGACGCTGACACGATG----- 515	
Qy	84 ProLeuGluIleValTyrGlnProLeuThrIleProAspProTyroGlnLeuGluIlaA 103	
Db	516 -----AAGTACAAACCGGTGAGCTGCGAAATCTTACAGTGTGGACCTGGC 563	
Qy	104 PhelIleLeuPheLysGluSerAspAlaAspProAlaAsnSerThrGluLysArgPheIle 123	
Db	564 TTCAAGCTTTCAGGGAACATGATCTAACCTGCGCTGAGGATGAGTGGCTCG 623	
Qy	124 MetArgPheIleArgGlyLysAsnIleSerTyrPheHisIleAspLeuValPheAsnLeu 143	
Db	624 ATGGCGTTGAGG-----ASCAGCCACGGGACTACCATGACTTGTGTTAGCTGTC 677	
Qy	144 GluLysAsnIleAlaThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163	
Db	678 AAGAAGAGATGTTGAGGCACTGAGAACATACTGCGATGCTGAGACTTCGATCGCAGTAC 737	
Qy	164 LeuTyrMetAlaThrLeuTyrLysThrIleThrAsnValAspGluPheGlyAlaser 183	
Db	738 TTCTACATGACTACGGTTGACTACAGACTAACCTGACCTTGACCGCTCAG 797	
Qy	184 PhePheAsnLysLeuSerPheThrThrGlyIlePheGlyTyrPheGlyIleLysArgAlaLeu 203	
Db	798 TTCTCAACAAAGCTTGCTTCACACTCGCTGTCGGTTGGTACCGAAGCGCTG 857	
Qy	204 LysGlnIleLeuArgSerAsnLeuProLeuAspIleGlyTyrPheGlyIleLysArg 223	
Db	858 AAGCGTTGTTAGGCAACCTTCGGTGAACCTGACCTGAGCCAC 914	
Qy	224 LeuGlnHistLeuSerSerTyrLysAspTyrMetAspPheGlyIlePheAlaLeuPro 243	
Db	915 ATCCGGAAATAGCTAGCGCTACCGCAGCATGATGACCGACAGCTGGCTCG 974	
Qy	244 LysPheAlaLysArgPheAspLeuMetValGlnArgLeuLeuAlaThrValAlaGly 263	
Db	975 TCGTTCGCTAGGCTTGTCTCAAGATGGCTACTAACTGCTGTTACGGTCAGCG 1034	
Qy	264 TyrValAspThrProTrpTyrLysIlePheAspMetLysIleUlysAsnPhMeValAsn 283	

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		Query Match:	32.66%	Indels:	43
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Qy	284 ArgWalphelebrOrthrLyslysphetherAsnlysGluIeargGluProserlys---	302			
Db	1095 ---TrCTTACTGACCCCTGCCAACATGTTGAAAGCAGCTCTCGACCTGTAAGACT	1151			
Qy	303 AlaleulysGlutysValSerThrAspThrLyslysphetherAsnlysGluIeargGluProserlys---	322			
Db	1152 GCTTACACAAAGCTGGCCCGAGAGCACAGCAGCTATCGGAAGTGTGCGGCAGCA	1211			
Qy	323 GlyThrvalAspPheAsnlysGluIeargGluProserlysAlaleulysGlutys	342			
Db	1212 AGGACCAAGCATTTGCCAAC--GGCTTACGGATTGGCANGGATGATTANGAG--	1265			
Qy	343 ValSerAsnAspAlaLysAspIepleuPheGluAsnlysIle-----Gly	356			
Db	1266 -----CCTACCCAAATAATTGTTGAGAAGCTGCTCACTACCTTCTAAGCA	1316			
Qy	357 GlyGlyThrvalAspPheleAsnlysGluIeargGluProserlysAlaleulysGlu	376			
Db	1317 AAGGAGGCCGTTGACAGCTGTTGACAGGTAA-----TCAAACATTGAGAG	1370			
Qy	377 LysValSerThrGlyAlaGluAspIepleuPheGluIe-----Lysle	390			
Db	1371 CGCTCTGGAAGTCGGAAGAATTCTCAAGGA	1430			
Qy	391 GlyGlyThrvalAspAlaLysAsnGlu	401			
Db	1431 TCACAAATAATTGAGATGCCGAAAGTAGTAG	1463			
RESULT	22				
LOCUS	A16434	1371 bp	DNA	linear	PAT 23-MAR-1994
DEFINITION	(lambda GEM-11 #9) gene 2 encoding a 211B4/rhoptry protein homologue.				
ACCESSION	A16434				
VERSION	A16434.1				
KEYWORDS					
SOURCE					
ORGANISM	Babesia canis				
Babesia; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;					
REFERENCE	1 (bases 1 to 1371)				
AUTHORS					
TITLE	BABESIAL ANTIGENS				
JOURNAL	patent: WO 9314204-A 13 22-JUL-1993;				
FEATURES					
source	1. .1371 /organism="Babesia canis" /db_xref="txon:5867"				
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BASE COUNT	418	a	312	c	325
ORIGIN			9		316
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Score:		Conservative:	95		
Percent Similarity:	55.65%				
Qy	301 SerlysAlaleulysGlutysValSerThrAspThrAspIepleuPheGluAsnlysIle	320			
Db	988 -----ACCAGGAGTCTCTGTTGACAGATC	1014			
Qy	321 GlyGlyThrvalAspPheAsnlysGluIeargGluProserlysAlaleulys	340			
Db	1015 CATGAACCCCACCAAGGAGTTCTGTGACAGATCCATGAAACCCAC-	1062			

	Query Match:	32.66%	Indels:	43
	DB:		Gaps:	9
Qy	341 GluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrVal 360			
Db	1063 -----AAGGTGTTCTGGTGAACRAGCCTCATGACCCACCAAG 1101	US-09-807-459-2 (1-458) x BBORHPCN (1-2796)		
Qy	361 AspPheIleAsnAsnGluLeuArgAspProSerLysAlaLeuIleArgLysValSerThr 380			
Db	1102 GAGTCTTCGTCGAACAAAGCTCCATGAAACCACCAAGAGGTCTCTCTAACATGTCACCC 1161	Qy 1 MetAlaProSerAspSerValGlyLysPheValThrIleLeuAlaAlaSerGluSer 20		
Qy	381 GlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsn 400	Db 1120 CTTCTCAATTAGATGAGCGAAAGACCTTGTCATCCCTCTAACGTGACGCATCG 1179		
Db	1162 GGGSCTTCCAGAGATACTGAAAGGCGAGTGA 420	Qy 21 ValAspSerAlaAlaAsnAlaTyMeteIleAsnSerAspMetSerAspThrLeuSerAla 40		
Qy	421 PheGluAsnIle-----GlyGlnGlyThrValAspIleAsnGlu 435	Db 1180 ACGAGGCGGTTAGAGGCTACAGAACTTGCAACTTCAACGGT 1239		
Db	1249 CTGAAATAGGCTGTAGAGGATGTCACATCAATGGGGATGTGACGATGTGAA 1308	Qy 41 ValSerAspAsnPheAlaGluArgTleCysSerGinValProLyserAspCyser 60		
Qy	437 IleArgAspPro-----SerLysAlaLeuIleArgLysValSerThrGlu 451	Db 1240 CGCAGGGAAAGGAGGAGGAGCTGICIGTGAACATCCGAGAGAGCTGAATGTCAG 1299		
Db	1309 ATGGGACTCCACATGAGCAGGCTCACAGAGATTAATGAGGTGGTACGAA 1368	Qy 61 AlaSerValSerAlaLeuIleArgLysValSerAlaIleGluSer 80		
RESULT 23		Db 1300 AAGAGCGTAGCTGAGTAGTGTGAAAGCTGCTCAGGTACTGCTTACATGAGAAC 1359		
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LOCUS	BBOBOPCN	Db 1360 CAGAGTACCCCTAACAGAGGAACATCACCSCGTCACGCCAACCTTACATG 1419		
DEFINITION	Babesia canis putative (60.2) rhoptry protein gene, complete cds.	Qy 101 GluAlaAlaPheIleLeuPheGluSerAspAlaAsnProAlaAsnSerThrGluLys 120		
VERSION	M91168.1 GI:155908	Db 1420 GAGGCCCGCTCTATGCTCTGAGAACAGCTGATCAACCCATTAACCCAAACGGAA 1479		
KEYWORDS	rhoptry protein	Qy 121 ArgPhePhePheArgLeuArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140		
SOURCE	Babesia canis (strain Townsville) DNA.	Db 1480 GCTTCGAGATGCGTTCGTCACGGGGAGCTTAATGGCCTATCACAAATTCCGGTC 1539		
ORGANISM	Babesia canis	Qy 141 AsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAla 160		
REFERENCE	1. (bases 1 to 2796)	Db 1540 AAATATCTATAAAACCTCTAGCATGGATGATGATAACCTCGAAGGTGTTGCA 1599		
AUTHORS	Dalrymple, B.P., Casu, R.E., Peters, J.M., Dimmock, C., Gale, K.R.,	Qy 161 SerArgTyrLeuTyroMetAlaThrIleTyrrTyrrLysThrThrAsnValAspGluPhe 180		
BASE, R. and Wright, I.G.		Db 1600 CGCAAAATATGCTTACATGCCACCTGATTAACAGACATACACCCCTTGATGTC 1659		
TITLE	Characterisation of a family of multi-copy genes encoding rhoptry protein homologues in Babesia bovis, Babesia ovis and Babesia canis mol. Biochem. Parasitol. 57, 181-192 (1993)	Qy 181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyIlePheGlyIlePheGlyIleLys 200		
JOURNAL		Db 1660 ATGCCAGGATCATACAAATGCTCTGCCACTGTTCGGAAGCAGATTAG 1719		
MEDLINE	93165069	Qy 201 ArgAlaLeuLysGlnIleLeuArgSerAsnIleProLeuAspIleGlyIleLys 220		
FEATURES	Location/Qualifiers	Db 1720 AACGCCCTAACGAAATTAATGCCACTAACATCCGACTTCGGC--AAGTCACAC 1776		
SOURCE	1. . 2796	Qy 221 ValSerArgLeuGlnIleThrSerSerTyrLysAspTyrMetAspIleGlnIlePro 240		
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Alignment Scores:	4.37e-53	Qy 281 MetValAsnArgValPheIleProThrLysIlePhePheAsnLysGluIleArgLysPro 300		
Pred. No.:	770..50	Db 1957 TTGTGAACTAACAGATCCATGAAACCCACCAAGGAGTCTCTGAAACAGATTCATGACCC 2016		
Score:	55..658	Qy 301 SerLysAlaLeuLysGluLysValSerThrAspPheThrLysAspLeuPheGluAsnLysIle 320		
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Db	1168	ATCGGAATTCTGCAGAATCCGCTAGGGATATAGATAGTAAATAAA-----	1221
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Db	1222	-----GCGAAGAAATTAGTCGCCGCAGCAG	1248
Qy	380	ThrGlyAlaGluaspLeuPheGluAsnLysIleGlyGinglyRlyThrValAspHeileasn	399
Db	1249	GACCGCCACAGGCATATGCGAGATCACGAAACCTGCTGAGTATACGAC	1308
Qy	400	-----AsnGluileArgaspProSerlysAlaLeuileargLysValAspHeileasn	414
Db	1309	GTTGTAAGAAGAATGATCTTGTGCACTAAC	1362
Qy	415	--ThrGluAlaAspaspLeuPheGluAsnLysIleGlyGinglyRlyThrValAspHeile	433
Db	1363	AGCTCTCAAGATGACAATAATGACAAAGAGACTGAGGAGGAAGTTGAGGAAGT	1422
Qy	434	AsnLysGluileArgaspProSerlysAla 443	
Db	1423	AAACCTGAGCTGAGCAAAAGAGTATCCT	1452
RESULT	25		
BBORHOP20V			
LOCUS	BBORHOP20V		
DEFINITION	Babesia ovis putative (60.4 and 60.5) rhoptry protein genes, 3' end	4145 bp	DNA
ACCESSION	M91169	and complete cds respectively.	linear
VERSION	M91169.1	GI:155900	INV 26-APR-1993
KEYWORDS	rhoptry protein.		
SOURCE	Babesia ovis (strain Ankara) DNA.		
ORGANISM	Babesia ovis		
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.			
REFERENCE	1 (bases 1 to 4145)		
Aralimpe, B.P., Casu, R.E., Peters, J.M., Dimmock, C., Gale, K.R., Böse, R. and Wright, I.G.			
TITLE	Characterisation of a family of multi-copy genes encoding rhoptry protein homologues in Babesia bovis, Babesia ovis and Babesia canis		
JOURNAL	Mol. Biochem. Parasitol. 57, 181-192 (1993)		
MEDLINE	93165069		
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Qy	201	ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyIhrGluIser	220
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Qy	221	ValSerArgLeuGlnHisIleThrSerSerTyrlsAspTyrmEtaspThrGlnIlePro	240
Db	2879	ATGGAACCTTATGTCATTGTCGAGGATACAGGACTACATGTCACAGTGCCA	2938
Qy	241	AlaLeuProLeuPheAlaLysArgPheSerLeuIleValGlnargLeuIleAlaThr	260
Db	2939	ACCTTCAAGTGTGCGAACCTTACACTGACGTTATGAAAGTTCCTGTCAGCAGC	2998
Qy	261	ValAlaGlyItyValAspThrProTrpTyrlsLysTrpTyrmEtaspThrGlnIlePro	280
Db	2999	CTCGCCGCTTGTGTCAGGCTCATGGTACAAGAGATGGTCATAGATTAAGCTCTG	3058
Qy	281	MetValAsnArg-----	287
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QY 362 PhelIeasnAsnGluIeargAspProSerLysAlaLeuIleArgLysValSerThrGly 381  
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RESULT 2B

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 KEYWORDS Rhoptry associated protein.  
 SOURCE Babesia divergens  
 ORGANISM Babesia divergens  
 Eukaryota; Alveodata; Apicomplexa; Piroplasmida; Babesiidae;  
 Babesia.

REFERENCE 1 (bases 1 to 1483)  
 AUTHORS Skuce, J., Mallon, T.R. and Taylor, S.M.  
 TITLE Molecular cloning of a putative rhoptry associated protein  
 JOURNAL Mol. Biochem. Parasitol. 77 (1), 99-102 (1996)  
 MEDLINE 66379225  
 REFERENCE 2 (bases 1 to 1483)  
 AUTHORS Skuce, P.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-APR-1995) Skuce P. J., Department of Agriculture for Northern Ireland, Veterinary Sciences Division, Stoney Road, Stormont, Belfast, Northern Ireland, BT4 1SD

FEATURES source

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 BASE COUNT ORIGIN Alignment Scores:

US-09-807-459-2 (1-458) x BDRHASPR (1-1483)

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 Db 233 GATAGCGTCTGAGCCATTTGAGACAGTCATTCGTCATGCCGCTATCCAGGAAGC 292  
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 Db 1103 TCTCTCTACTGAGGGGCATGGCACAAAGAGGTTCTCACTCTGGAAGAGATGTA 1162

OY	317 GluasnlysileGlyglnglyRvalaspPhePheAsnlysGluileargaspProSer 336       ::	ORIGIN
Db	1163 AACGAGAGATC--CTGTGTAAATTCTCAAGGACGGCATAGGAACAGCTCT 1219	Alignment scores:
RESULT	29	Pred. No.: 2.02e-35
AFO26272	AF026272 4414 bp DNA linear INV 03-NOV-1997	Length: 4414
LOCUS	Babesia bigemina Rap-1c (rap-1c) gene, complete cds, and	Matches: 147
DEFINITION	YJR070c-like protein (YJR070c-like) gene, partial cds.	Conservative: 80
ACCESSION	AF026272	Best Local Similarity: 28.71%
VERSION	AF026272.1 GI:2583051	Mismatches: 177
KEYWORDS		Indels: 108
SOURCE	Babesia bigemina.	Gaps: 15
ORGANISM	Babesia bigemina	
REFERENCE	Babesia.	
AUTHORS	Hetzl, I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.	
TITLE	Genomic cloning of Babesia bigemina rap-1c gene	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 4414)	
AUTHORS	Hetzl, I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.	
TITLE	Direct Submission	
JOURNAL	Submitted (22-SEP-1997) Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164-7040, USA	
FEATURES		
source	Location/Qualifiers	
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BASE COUNT	1213 a 1030 c 1087 g 1082 t 2 others	
OY	1 METAlaProSer-----AspSerValGlyAspValThrysthr 13       ::	
Db	1117 ATGGCCCTGACACTGTGAGCTGCCGTTGATCCCCGCGACGACGACGACGACG 1176	
OY	14 LeuLeuAlaAlaSerGluSerValAspSerAlaAlaAlaAsnAlaTyrMetIleAsnSerAsp 33     ::        ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1177 CTCCTCGAGAACGACAGCACAGATGAGAAGGCC----- 1209	
OY	34 MetSerAspTyrLeuSerAlaValSerAspSerPheAlaGluArgIleCysSerGlnVal 53     ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1210 ATGCAGGAGAAATCGGACTGATCAACGATGACTCCATTSCCGAATAATGTCCTCGGCAGC 1269	
OY	54 ProLySlySerAsnCysSerAlaSerValSerAlaTyrMetSerArgCysAlaTyr 73 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1270 AAGGAGGAGCACCATGCGCATGCAAATCCTGCTACAGTGCGCTTCAAGGCCAAC 1329	
OY	74 AspCysLeuThrLeuGlnSerLeuLysTyrProLeuGluAlaLysTyrGlnProteuthr 93 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1330 ACTGCTCACCACATCGATGCCGCGAACACGCCAACACGCCAACACGCCAAC 1389	
OY	94 LeuProAspProTyrglnLeuGluAlaAlaPheIleLeuPhyLysGluSerAspAlaAsn 113     ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1390 CTGCGCTGACCCCTACCACTACGAGCTCACGCCGCGTCCGCTGTCAGACTGCCGCCAAC 1449	
OY	114 ProAlaAsnSerThrGluLysArgPheTrpMetArgPheArgGlyLysAsnHisSer 133 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1450 GAGGAGGAGCACTGGATGGCATGGCTTCAGGGGGCGCTACGCT 1509	
OY	134 TyrPheHisAspLeuValPheAsnLeuLeuGluLysAsnValThrArgAspAlaAspAla 153 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1510 GCTTACTACAGCTTCACCCCTCACCTGAGGCCAACCTGCTCTCGGCCGACGACA 1569	
OY	154 ThrAspIleGluAsnSerAspAspSerArgTyrLeuTyMeteAlaThrLeuTy-Tylysthr 173     ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1570 ATAGCCCTGATGGCTTCGTCAGAAGACTCTACATGCCCTAACATGCCCTGGCGAACAC 1629	
OY	174 TyrThrAsnValIleAspGluPheDiyalaSerPhePheAsnLysLeuSerPheThrThrGly 193     ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1630 TACTGTCGCTGATGGCTACACGCCAAATATTACATGCCCTGGCGAACAC 1689	
OY	194 LeuPheGlyTrpGlyIleLysArgAlaLeuLysGlnIleLeuLysSerAsnLeuProLeu 213 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1690 ATCTGGACCTTAAGATCAAAAGGGCTTGAGGAGATCCTGCTGAGGCCAACAGCGGAGC 1749	
OY	214 AspIleGlyIleGluIleSerValSerArgLeuGluIleThrSerSerTyrLysAsp 233 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1750 GGCCTC--CAAGCGAACGAGCTCAAGCCATACGCCCTGCTGCTACGGCTACAGCG 1806	
OY	234 TyrMetAspThrGlnIleProAlaLeuProTyrPheAlaLysArgPheSerIleMetVal 253     ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1807 TACATGCCACCAACGCCAACGCCGTCCTGCCCTACGGCTCTCGANGGTC 1866	
OY	254 ValIleGluLeuAlaThrValAlaGlyIleValAspIleProTyrIleLysTyr 273     ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1867 GTCACGGCTCTGGGACAACCTCACGGGCTTAACGAGGCCGTTCAAGGCTTG 1926	
OY	274 TyrMetIleLeuLysAsnPhenylmetValAsnArgValPheIleProTyrIleLysPhe 293 ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::    ::	
Db	1927 TTGGAAAGTGAGAACCTCTCACGGTAGCAA----CCAGCGAACGCCAC 1980	
OY	294 AsnLysGluIleArgGluProSerLysAlaLeuLysGluLysValSerThrAspThrLys 313	

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Db 1981 -----GAAATGCGAANACCATGCCACCGAGGAGG----- ACCCAG 2019  
Qy 314 AspLeuPheGluasnLysIleGlyLngIlyThrValAspPheAsnLysGluIlearg 333  
Db 2020 CCTCTCGAGGAAATAAG-----TCAGTTTGCAAG----- 2052  
Qy 334 AspProSerLysAlaLeuLysGluLysValSerAsn----- 345  
Db 2053 -----GTCAAGGAAGCTGGCAACATCGCTTCAACACGGCATTTC 2097  
Qy 346 -----AspAlaLys----- 348  
Db 2098 CGAAGGGTGAGCCAAAGACTCCCTCACCGCAGCAGGACATTATGGCAGC 2157  
Qy 349 -----AspLeuPheGluasnLysIleIly 356  
Db 2158 TTGTGTCGCGCTGATGCGCTGCTGAGCGGGGTCAGTCAGTGGAG---AAAGAGGC 2214  
Qy 357 GlycylThrValAspPheIleAsnAspGluIleArgAspProSerLysAlaLeuIlearg 376  
Db 2215 GAACCTCGA-----AACGAGGAGGTGACCGCAGTGGCCCGGCTCC 2262  
Qy 377 LysValSer-----ThrGlyAlaGluAspIeu 385  
Db 2263 AAGGGCCCTGAGAGTGAATGGCGAAGTCGCAGACCAAGTAGATGAGTGGGCTTCACCTG 2322  
Qy 386 PheGluAsnLysIleGlyGln-----GlyThrValAspIphe 397  
Db 2323 GCTCAACCGAATGGCGAGAGGAGCTCTCGAACGCTCTAAAGGCCGACGATGG 2382  
Qy 398 IleAsnAsnGluIleArgAsp-----ProSerLysAlaLeuIle 410  
Db 2383 ATGGACGAGATGGGAGGACCCGAATCTGACGAGTTGCCAAGAGGGCT 2442  
Qy 411 ArgGlyValTyrrhGlulaAspAspLeuPheGluAsnLysIleGlyLngIlyThrval 430  
Db .2443 AACCTCTAACGACAGGCTACACAAAAGTCTGAGAACATCTTGGACACCGGGGCAATT 2502  
Qy 431 AspPheIleAsnLysGluIleArgAspProSerLys 442  
Db 2503 AAGGGATGGCGTAGCCGATCGGGTCCGAGAAG 2538

RESULT 30

AF014757 AP014757 575 bp DNA linear INV 31-JAN-2001  
LOCUS Babesia bigemina CGA rap-1 alpha (rap-1) gene, partial cds.  
DEFINITION AF014757 GI:2429255  
ACCESSION AF014757.1  
VERSION AF014757.1 GI:2429255  
KEYWORDS  
SOURCE Babesia bigemina.  
ORGANISM Babesia bigemina.  
Babesia. Alveolata; Apicomplexa; Piroplasmida; Babesiidae;  
Babesia.  
REFERENCE 1 (bases 1 to 575)  
AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.  
TITLE Genetic variation in the dimorphic regions of RAP-1 genes and rap-1 loci of Babesia bigemina  
JOURNAL Mol. Biochem. Parasitol. 90 (2), 473-489 (1997)  
MEDLINE 98135662  
REVERSE 2 (bases 1 to 575)  
AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.  
TITLE Submitted (16-JUL-1997) Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164-7040, USA  
JOURNAL  
FEATURES source  
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Qy 314 AspLeuPheGluasnLysIleGlyLngIlyThrValAspPheAsnLysGluIlearg 333  
Db 2020 CCTCTCGAGGAAATAAG-----TCAGTTTGCAAG----- 2052  
Qy 334 AspProSerLysAlaLeuLysGluLysValSerAsn----- 345  
Db 2053 -----GTCAAGGAAGCTGGCAACATCGCTTCAACACGGCATTTC 2097  
Qy 346 -----AspAlaLys----- 348  
Db 2098 CGAAGGGTGAGCCAAAGACTCCCTCACCGCAGCAGGACATTATGGCAGC 2157  
Qy 349 -----AspLeuPheGluasnLysIleIly 356  
Db 2158 TTGTGTCGCGCTGATGCGCTGCTGAGCGGGGTCAGTCAGTGGAG---AAAGAGGC 2214  
Qy 357 GlycylThrValAspPheIleAsnAspGluIleArgAspProSerLysAlaLeuIlearg 376  
Db 2215 GAACCTCGA-----AACGAGGAGGTGACCGCAGTGGCCCGGCTCC 2262  
Qy 377 LysValSer-----ThrGlyAlaGluAspIeu 385  
Db 2263 AAGGGCCCTGAGAGTGAATGGCGAAGTCGCAGACCAAGTAGATGAGTGGGCTTCACCTG 2322  
Qy 386 PheGluAsnLysIleGlyGln-----GlyThrValAspIphe 397  
Db 2323 GCTCAACCGAATGGCGAGAGGAGCTCTCGAACGCTCTAAAGGCCGACGATGG 2382  
Qy 398 IleAsnAsnGluIleArgAsp-----ProSerLysAlaLeuIle 410  
Db 2383 ATGGACGAGATGGGAGGACCCGAATCTGACGAGTTGCCAAGAGGGCT 2442  
Qy 411 ArgGlyValTyrrhGlulaAspAspLeuPheGluAsnLysIleGlyLngIlyThrval 430  
Db .2443 AACCTCTAACGACAGGCTACACAAAAGTCTGAGAACATCTTGGACACCGGGGCAATT 2502  
Qy 431 AspPheIleAsnLysGluIleArgAspProSerLys 442  
Db 2503 AAGGGATGGCGTAGCCGATCGGGTCCGAGAAG 2538

Alignment Scores:  
Pred. No.: 1.24e-34 Length: 575  
Score: 532.00 Matches: 103  
Percent Similarity: 69.23% Conservative: 32  
Best Local Similarity: 52.82% Mismatches: 52  
Query Match: 22.55% Index: 8  
DB: 3 Gaps: 2

US-09-807-459-2 (1-458) x AF014757 (1-575)

Qy 4 SerAspSerValGlyAspValThrLysThrLeuAlaLysSerGluSerValAspSer 23  
Db 14 GCAGAGGTGGTGGAGATCTGTCAGAACCTTGCTGGAGGCCATGAGGTGTCATCT 73  
Qy 24 AlaAlaAsnAlaAlaTyrMetIleAsnSerAspMetSerAspTyrIleSerAlaValSerAsp 43  
Db 74 GAATGGGCAACTCAGTCACAAAGATATGCCAAACTCAATTGCTCAATGCTAAAG 133  
Qy 44 AspNpheAlaGluArgIleGlySerGlnAlaProLygIysSerAsnCysSerAlaSerAl 63  
Db 134 ACCATGTTGGTGGAGGTCTGGAGAACGTGCTGGAAACTCTACTGGGGTGGAGGCTA 193  
Qy 64 SerIaTATyMeteSerArgCysAlaLysGlnAspCysLeuThrIeugInserCuleyTyr 83  
Db 194 ATGGCTATGTTAACGGTGTGATGAGGGATGTCGAGCTGACGATGACGATG----- 247  
Qy 84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProSpProtYrgIleGluGuaIala 103  
Db 248 -----AAGTACAAGCCGTTGAGTCGCAAATCTTACCATGAGTTGGACGCTGCC 295  
Qy 104 PhelLeuPhelPhyGluSerAspAlaAsnProLysSerThrGluLysSerGlySerGlySer 123  
Db 296 TTCACTGCTTTCAGGGAAGGTCTAACCTCGAGAATGAGGTGAAACCCCTCTGG 355  
Qy 124 MetArgPheArgArgGlyLysAsnHisseryTyrPheHisAspIleAla 143  
Db 356 ATGGCTGTCGAG-----AGCAGCCACGGGACATACCATCAGCTTGTGTTGTTG 409  
Qy 144 GluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163  
Db 410 AAGAGAAATGTTGAGCGACCTGAAATCCATGAGTTGGAGACTTCGCACTGCACTG 469  
Qy 164 LeuTrpMetAlaThrLeuThrTrpIleTrpIleTrpIleTrpIleTrpIleTrpIle 183  
Db 470 TTCTPACAGTACTAGTGTGACTACAGACTTACCTGACGCGTGACTTACGGGGCTAAG 529  
Qy 184 PhePheAsnLysIleSerPheThrThrGlyLeuPheGlyLrpGly 198  
Db 530 TTCTCAACAGCTTGTCTCACACTCGCTGTTGGTCTGGT 574

RESULT 31

AF014758 AP014758 575 bp DNA linear INV 31-JAN-2001  
LOCUS Babesia bigemina CGP rap-1 alpha (rap-1) gene, partial cds.  
DEFINITION Babesia bigemina CGP rap-1 alpha (rap-1) gene, partial cds.  
ACCESSION AF014758  
VERSION AF014758.1 GI:2429257  
KEYWORDS  
SOURCE Babesia bigemina.  
ORGANISM Babesia bigemina.  
Babesia. Alveolata; Apicomplexa; Piroplasmida; Babesiidae;  
Babesia.



	Best Local Similarity:	52.82%	Mismatches:	52
Query Match:	22.55%	Indels:	8	
DB:	3	Gaps:	2	
US-09-807-459-2 (1-458) x AF014762 (1-575)				
QY 194 ATTCGCTATGTTAACGGTTGTGATGAGGGGATTCGCGCTGACAGCATG----- 247				
QY 84 ProLeugluAlaLysIstyrglnproLauthrLeuproAspProtYrlnLeugluAla 103				
Db 248 -----RAAGTACAAGCGGTGAGCTGCTGCCAATCTTACCGATGAGCGCTGCC 295				
QY 104 PhelLeupheLysGluserAspalaAsnSerthrGlyArgPheTrp 123				
Db 296 TTCACTGCTTTCAGGGAAGTGCTAACCTGCGAAGATGAGGTGAAAGCCTCTGG 355				
QY 124 MetArgPheArgGlyLysAsnHisSerThrPheHisAspLeuValPheAsnLeu 143				
Db 410 AGAAGAATGTTGACCGCACCTGTGATCATGATGTTGAGACTTTCGCAATCGCAGTAC 469				
QY 356 ATGCCTGAGG-----AGCAGCACGGGCACTACATCACTTGTGTTAGCTGTTG 409				
QY 144 GluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163				
Db 470 TTCTACATGACTACGGTACATAAGACTTACCTGACGTTACCGGCTTAAG 529				
QY 184 PhePheAsnLysLeuSerPheThrThrGlyLeupheGlyTrpGly 198				
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RESULT 33				
LOCUS AF014762 575 bp DNA linear INV 31-JAN-2001				
DEFINITION Babesia bigemina rap-1 alpha (rap-1) gene, partial cds.				
ACCESSION AF014762.1 GI:2429265				
VERSION .				
KEYWORDS .				
SOURCE .				
ORGANISM Babesia bigemina.				
FEATURES .				
REFERENCE .				
AUTHORS Hotzel, T., Suarez, C.E., McElwain, T.F. and Palmer, G.H.				
TITLE Genetic variation in the dimorphic regions of Rap-1 genes and rap-1 loci of Babesia bigemina				
JOURNAL Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)				
MEDLINE 98135662				
REFERENCE .				
AUTHORS Hotzel, T., Suarez, C.E., McElwain, T.F. and Palmer, G.H.				
TITLE Direct Submission				
JOURNAL Submitted (16-JUL-1997) Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164-7040, USA				
FEATURES .				
REFERENCE .				
SOURCE 1. (bases 1 to 575)				
Hotzel, T., Suarez, C.E., McElwain, T.F. and Palmer, G.H.				
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TIVGEVCEKVKAGNSICGEGSIVAYVNRCDGCLTDMSMKRPLSPNPKDQAALMF				
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LYVKTLYTWDFTAKKFNLKAFTRFLFGC"				
BASE COUNT ORIGIN 145 a 119 c 153 g 158 t				
Alignment Scores: 1.24e-34 Length: 575				
Pred. No.: 532.00 Matches: 103				
Score: 62.23% Conservative: 32				
FEATURES .				
REFERENCE .				
SOURCE 1. (bases 1 to 575)				
Hotzel, T., Suarez, C.E., McElwain, T.F. and Palmer, G.H.				
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/organism="Babesia bigemina"				
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ORIGIN		RESDPNPKNEVKRFWRSRSSHGDYHHEVVSLLKKNVYRDPESENDVNFAASYFMT	
Alignment Scores:			
Pred. No.:	1.24e-34	Length: 575	
Score:	532.00	Matches: 103	
Percent Similarity:	69.23%	Conservative: 32	
Best Local Similarity:	52.82%	Mismatches: 52	
Query Match:	22.55%	Indels: 8	
DB:	3	Gaps: 2	
US-09-807-459-2 (1-458) x AF014768 (1-575)			
Qy	4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaLaserGluSerValAspSer	23	
Db	14 GCAGAGGTGGTGGAGATGTCGCCAGACCTTGCTGGAGGCCATAGGAGTTGTCATGCT	73	
Qy	24 AlaIaAsnAlaTyrMetIleAsnSerAspMetSerAspIleSerAspYleSerAsp	43	
Db	74 GAAATGGAAGCAACTCAGGTCACAAAGATGCAAGTCAATTGCTAATGTTAGGAG	133	
Qy	44 AsnPheAlaGluArgleCysSerGlnValProlylGlySerAsnCysSerAlaSerVal	63	
Db	134 ACCATGTTGGTGGAGCTCGAGGAAAGCTTACCTGGCTGGAGCTGTA 193		
Qy	64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuThrTyr	83	
Db	194 ATTGCCTATGTTAACGTTGGTGGAGGAGCATGTCGAGCTGACAGCATG	247	
Qy	84 ProLeuGluLalaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAla	103	
Db	248 ---AGTACAAAGCCGTGAGTCGCAAAATCCTTACCGAGTGGAGCTGCC 295		
Qy	104 PheIleLeuPhelysGluSerAspAlaAsnProAlaAsnSerThrGluIysArgThrPhe	123	
Db	296 TTGCACTCTTTCAGGAAAGCTGATCTACCCCTGGAAAGATGAGCTGAAAGCCTG 355		
Qy	124 MetArgPheArgArgLysAsnHisSerTyrPheHisAspLeuValPheAsnIleLeu	143	
Db	356 ATGCCTGTCGAGG-----ACGAGCACGGGACTACCATCTGTTGCTTAGCTGTG 409		
Qy	144 GluIysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr	163	
Db	410 AAGAGAAATGTTGACGGACCCCTGATCCATGATGTTGAGAACITCGCATCGCAGTAC 469		
Qy	164 LeuTyrMetAlaThrLeuTyrTyrIysThrTyrThrAsnValAspIleGluPheGlyAlaSer	183	
Db	470 TTCTCATGACTGCTGGTGTGACTACAGACTAACCTGACCTGTTAGGGCTTAAG 529		
RESULT 35			
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LOCUS	Babesia bigemina S2P rap-1 alpha (rap-1) gene, partial cds.		
DEFINITION			
ACCESSION	AF014761		
VERSION	AF014761.1	GI:2429263	
KEYWORDS			
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	TIVGEVCEKYGAGNSPGESVIAVYNRCDEDCLTUDSMKYKPLSLPNPQOLDRAFMF		
	RESDPNPKNEVKRFWRSRSSHGDYHHEVVSLLKKNVYRDPESENDVNFAASYFMT		
BASE COUNT	145 a 119 c 153 g 158 t	TLYKTYLTDFTAKFFKNLAKFTTRLGFG"	
ORIGIN		RESDPNPKNEVKRFWRSRSSHGDYHHEVVSLLKKNVYRDPESENDVNFAASYFMT	
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 Cds 1 (bases 1 to 575)  
 Authors Hotzel, I., Suarez, C.E., McElwain, T.F. and Palmer, G.H.  
 Title Genetic variation in the dimorphic regions of RAP-1 genes and rap-1 loci of Babesia bigemina  
 Journal Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)  
 Medline 98135662  
 Reference 2 (bases 1 to 575)  
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 Title Direct Submission  
 Journal Submitted (16-JUL-1997) Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164-7040, USA  
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||| ||||| ||||| ||||| ||||| |||||  
 Db 365 GAAATGGAAGCAGCTCAGATTACGAAGATATGAGATTCAGTTGGCGAACGTCAAGAG 424  
 Qy 44 AsnpheAlaGluArgAglleucySerGlnValProlySlySerAsnCysSerAlaSerVal 63  
 :::  
 Db 425 ACCATCGTGTGATGGCTCGCAGAAAAGATGCCTGAAAGCCTAGTGCGCAAGAGCGTA 484  
 Qy 64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrIleUglnSerLeuLysTyr 83  
 :::  
 Db 485 ATTGCCTATGTTGACCGTGTGATGAGGGCATGTCGACGCTGACGCCATG----- 538  
 Qy 84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAla 103  
 :::  
 Db 539 -----AACTACAGCCGTTGAGCTGCGCAATTCTAACAGTGTGAGCTGCC 586  
 Qy 104 PheIleLeuPheLysGlusSerAspAlaAsnProAlaAsnSerTyrGluLysArgPheTrp 123  
 :::  
 Db 587 TTCTTGCTTTCAGGAAGTGTCTAACCTCGCAGATGAGTGTGCTTCGG 645  
 :::  
 587 TTCTTGCTTTCAGGAAGTGTCTAACCTCGCAGATGAGTGTGCTTCGG 645  
 Qy 124 MetArgPheArgArgGlyLysAshisSerTyrPheHisAspLeuValPheAsnLeuLeu 143  
 :::  
 Db 647 ATGGCTTCGAGG----ACCAGCCACGGGGACTACCATCACTTGTGTTAGCTTGTG 700  
 :::  
 647 ATGGCTTCGAGG----ACCAGCCACGGGGACTACCATCACTTGTGTTAGCTTGTG 700  
 Qy 144 GluLysAsnValThrArgAspAlaAspAlaThrSpIleLuanPheAlaSerArgTyr 163  
 :::  
 Db 701 AAGAGAAATGTTGACGGACCTGCAATCCAATGATGTTGAGAACTTGCATCCAGTAC 760  
 :::  
 Db 164 LeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSer 183  
 :::  
 761 TTCTCACATGACTAGTGTGACTACAGACTTACCTGACCTTGACTTACGCCGCTAG 820  
 :::  
 Qy 184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGly 198  
 :::  
 Db 821 TTCTCAACRAGCTTGCTTCACACTCGCCGTCGGTTTCGGT 865

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 Job time : 1978 secs

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